## Claims

What is claimed is:

1. A method of constructing a profile of intronic regions from a given taxonomic group of organisms, said profile being useful for characterizing target organisms, comprising the steps of:

(a) selecting at least one intronic region known to be found in some or all members of the taxonomic group;

(b) analyzing the intronic region of known members of the taxonomic group; and

(c) constructing a profile of intronic region characteristics from the taxonomic group, wherein the profile is capable of being used to characterize the target organism.

2. The method of claim 1, wherein the intronic region comprises at least one exon, and wherein the step of selecting an intronic region further comprises aligning the exon.

3. The method of claim 1, wherein the target organism is suspected of belonging to a smaller taxonomic group than the given taxonomic group.

4. The method of claim 3, wherein the profile is constructed of intronic region characteristics from a class or subclass of organisms, and wherein the target organism is suspected of belonging to a single genus or related genera.

5. The method of claim 1, further comprising the step of determining the presence or absence of the intronic region.

6. The method of claim 1, wherein the step of analyzing the intronic region further comprises the steps of:

(i) choosing a pair of intronic region-specific primers suitable for amplifying the intronic region;

(ii) performing a primer extension reaction to generate primer amplified products; and

(iii) analyzing the amplified products.

7. The method of claim 6, further comprising the step of determining the length of the intronic region.

8. The method of claim 6, further comprising the step of determining the nucleotide sequence of the intronic region.

9. The method of claim 6, further comprising the step of analyzing the amplified products using restriction fragment length polymorphism.

10. The method of claim 6, further comprising the step of hybridizing the amplified products with specific nucleic acid probes.

11. The method of claim 6, wherein the intronic region-specific primers flank more than one intron insertion site.

12. The method of claim 6, wherein the intronic region-specific primers flank a single intron insertion site.

13. The method of claim 6, wherein the target organisms are eukaryotes.

14. The method of claim 13, wherein the eukaryotes are fungi.

15. The method of claim 14, wherein the fungi are of the genus *Candida* or *Aspergillus*.

16. The method of claim 6, wherein at least one of the intronic region-specific primers is complementary to a sequence of nucleotides in an exon.

17. The method of claim 6, wherein at least one of the intronic region-specific primers is complementary to a sequence of nucleotides in an intron.

18. The method of claim 6, wherein the intronic region further comprises all or a portion of an open reading frame that encodes a protein.

19. The method of claim 18, further comprising the steps of:

(a) producing a protein encoded by the amplified product; and

(b) producing an antibody reactive with an antigenic determinant of the protein.

20. The method of claim 18, further comprising the step of analyzing the intronic region by assaying for enzymatic activity.

21. The method of claim 20, wherein the enzymatic activity is an endonuclease, maturase or reverse transcriptase activity.

22. A method of characterizing a target organism suspected of being a member of a given taxonomic group comprising the steps of:

(a) selecting at least one intronic region known to be found in some or all members of the taxonomic group;

(b) analyzing the intronic region of the target organism; and

(c) comparing it to known intronic region characteristics of members of the taxonomic group.

23. The method of claim 22, further comprising the step of determining the presence or absense of the intronic region.

24. The method of claim 22, wherein the step of analyzing the intronic region further comprises the steps of:

(i) choosing a pair of intronic region-specific primers suitable for amplifying the intronic region;

(ii) performing a primer extension reaction to generate primer amplified products; and

(iii) analyzing the amplified products.

25. The method of claim 24, further comprising the step of determining the length of the intronic region.

26. The method of claim 24, further comprising the step of determining the nucleotide sequence of the intronic region.

27. The method of claim 24, further comprising the step of analyzing restriction fragment length polymorphism of the intronic region.

28. The method of claim 24, further comprising hybridizing the amplified product with specific nucleic acid probes.

29. The method of claim 24, wherein the intronic region-specific primers flank more than one intron insertion site.

30. The method of claim 24, wherein the intronic region-specific primers flank a single intron insertion site.

31. The method of claim 24, wherein at least one of the intronic region-specific primers is complementary to a sequence of nucleotides in an exon.

32. The method of claim 24, wherein the amplification product is analyzed by hybridizing it to a nucleic acid probe.

33. The method of claim 22, wherein the organism is a eukaryote.

34. The method of claim 33, wherein the eukaryote is a fungi.

35. The method of claim 34, wherein the fungi is of the genus *Candida* or *Aspergillus*.

36. The method of claim 22, wherein the target organism is found in a sample from an animal or a plant source.

37. The method of claim 22, wherein the target organism is found in a sample from a human source.

38. The method of claim 22, wherein the intronic region further comprises all or a portion of an open reading frame that encodes a protein.

39. The method of claim 38, further comprising the steps of:

(a) producing a protein encoded by the amplified product; and

(b) producing an antibody reactive with an antigenic determinant of the protein.

40. The method of claim 39, further comprising the step of analyzing the intronic region by assaying for enzymatic activity.

41. The method of claim 40, wherein the enzymatic activity is an endonuclease, maturase or reverse transcriptase activity.

42. An isolated nucleic acid, comprising a sequence of nucleotides from nucleotide positions 31-1489 of SEQ ID NO: 29.

43. An isolated nucleic acid, comprising a sequence of nucleotides from nucleotide positions 31-1465 of SEQ ID NO: 33.

44. An isolated nucleic acid, comprising a sequence of nucleotides from nucleotide positions 42-1013 of SEQ ID NO: 37.

45. An isolated nucleic acid, comprising a sequence of nucleotides from nucleotide positions 31-321 of SEQ ID NO: 41.

46. An isolated nucleic acid, comprising a sequence of nucleotides from nucleotide positions 42-1009 of SEQ ID NO: 45.

47. An isolated nucleic acid, comprising a sequence of nucleotides from nucleotide positions 31-1423 of SEQ ID NO: 55.

48. A kit for characterzing a target organism suspected of being a member of a given taxonomic group, wherein at least one intronic region is known to be found in some or all members of the taxonomic group, the kit comprising at least one pair of intronic region-specific primers suitable for amplifying the intronic region and a profile of intronic region characteristics from the taxonomic group, wherein the profile is capable of being used to characterize the target organism.